

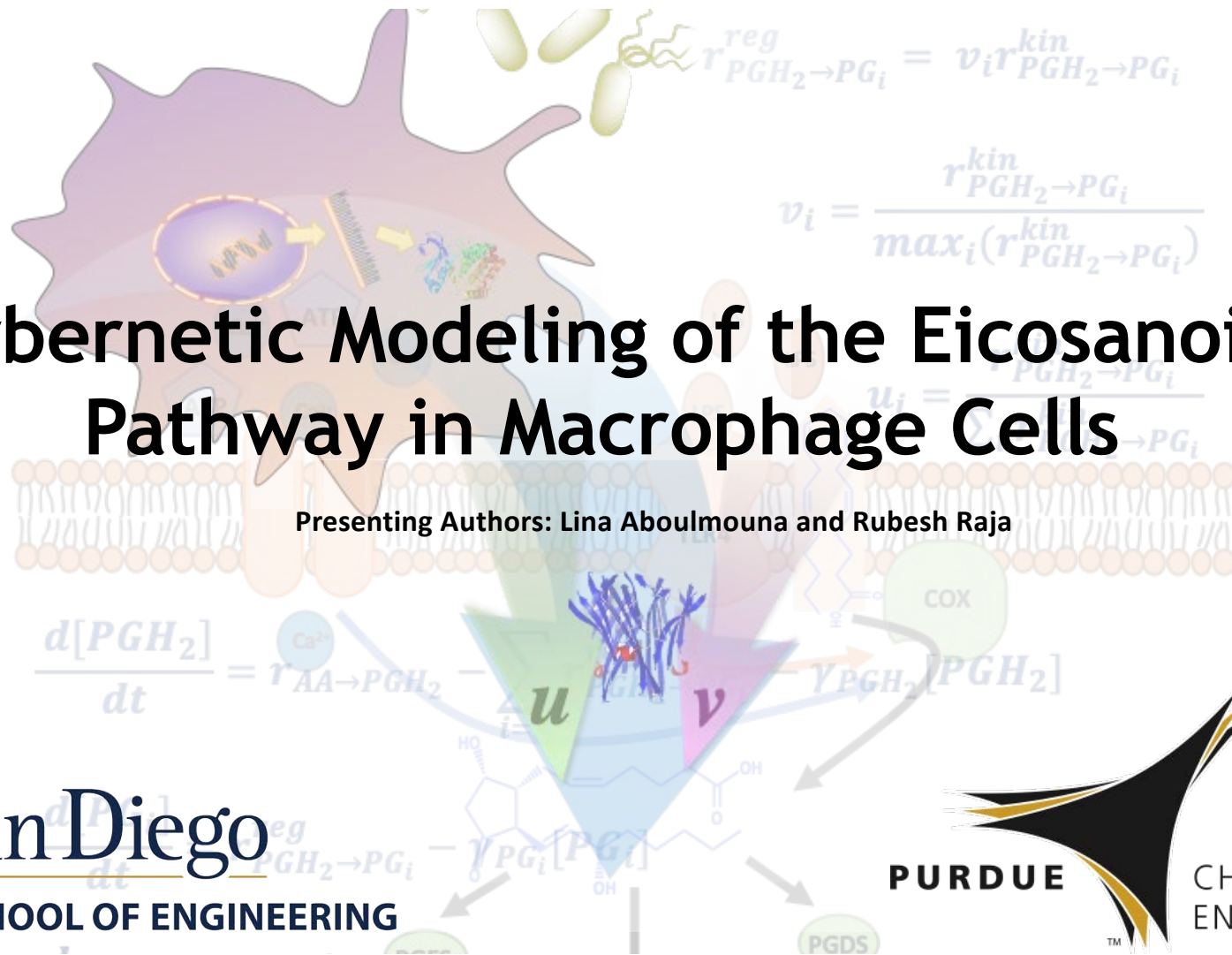
Cybernetic Modeling of the Eicosanoid Pathway in Macrophage Cells

Presenting Authors: Lina Aboulmouna and Rubesh Raja

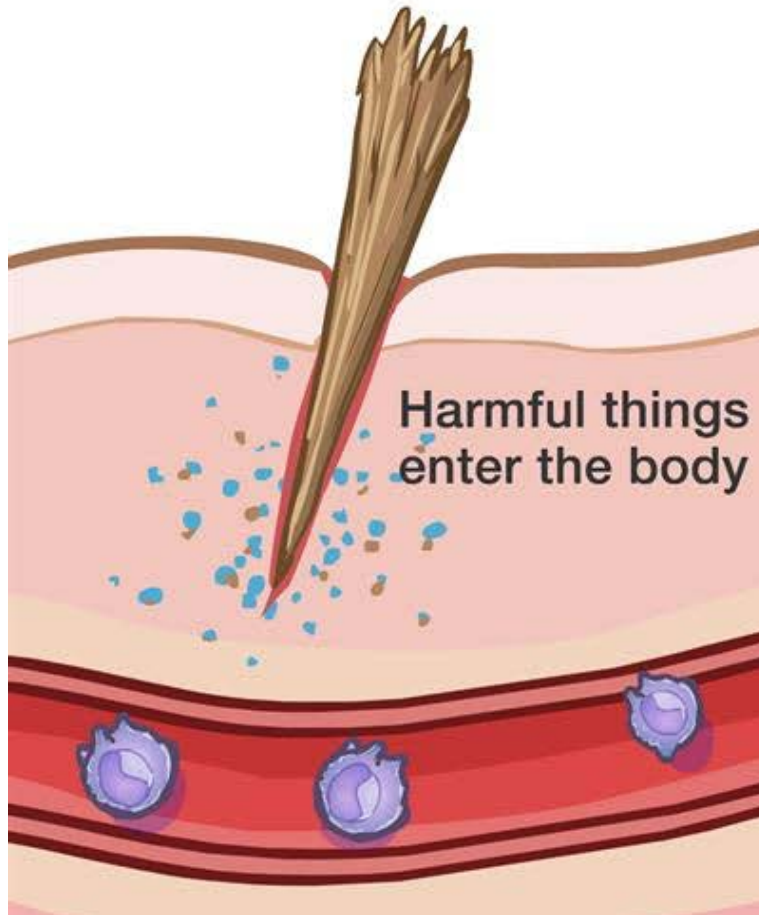
UC San Diego
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PURDUE

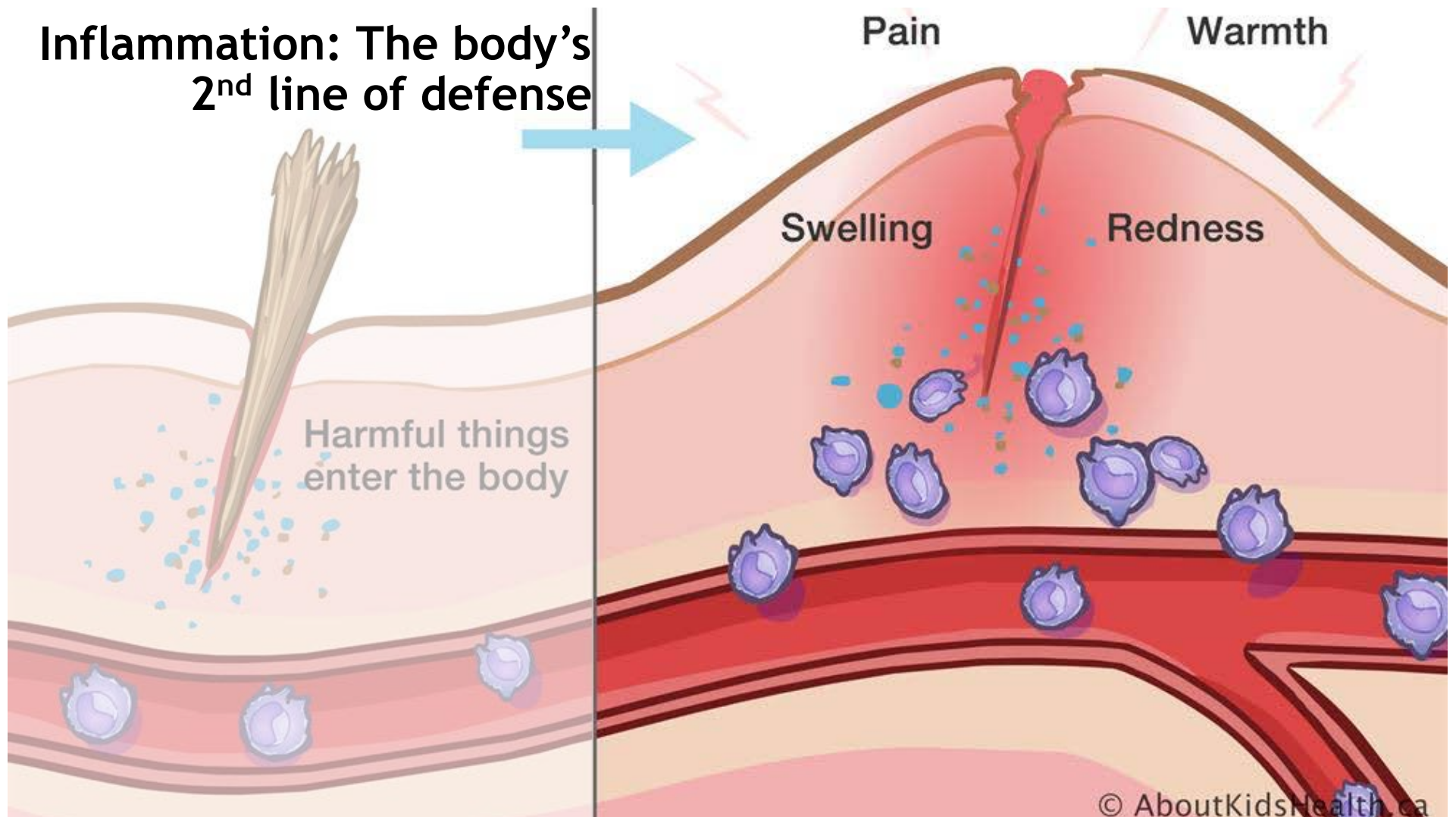
CHEMICAL
ENGINEERING



Inflammation: The body's 2nd line of defense



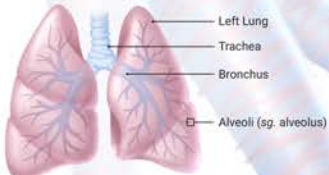
Inflammation: The body's 2nd line of defense



COVID-19

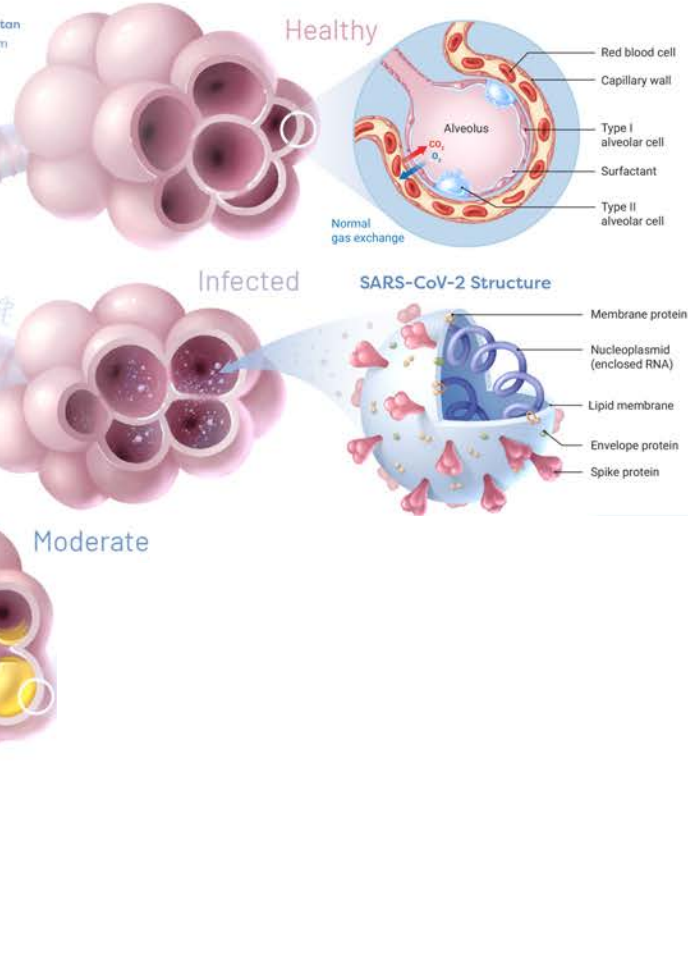
HOW DOES IT AFFECT YOU?

Coronavirus Disease 2019 (COVID-19) is a pandemic caused by Severe Acute Respiratory Syndrome Coronavirus 2, also called SARS-CoV-2. Despite the widespread awareness regarding COVID-19, many are still unaware about how it affects the human body.



SARS-CoV-2 starts its journey in the nose, mouth, or eyes and travels down to the alveoli in the lungs. Alveoli are tiny sacs of air where gas exchange occurs.

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@azuravesta
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COVID-19

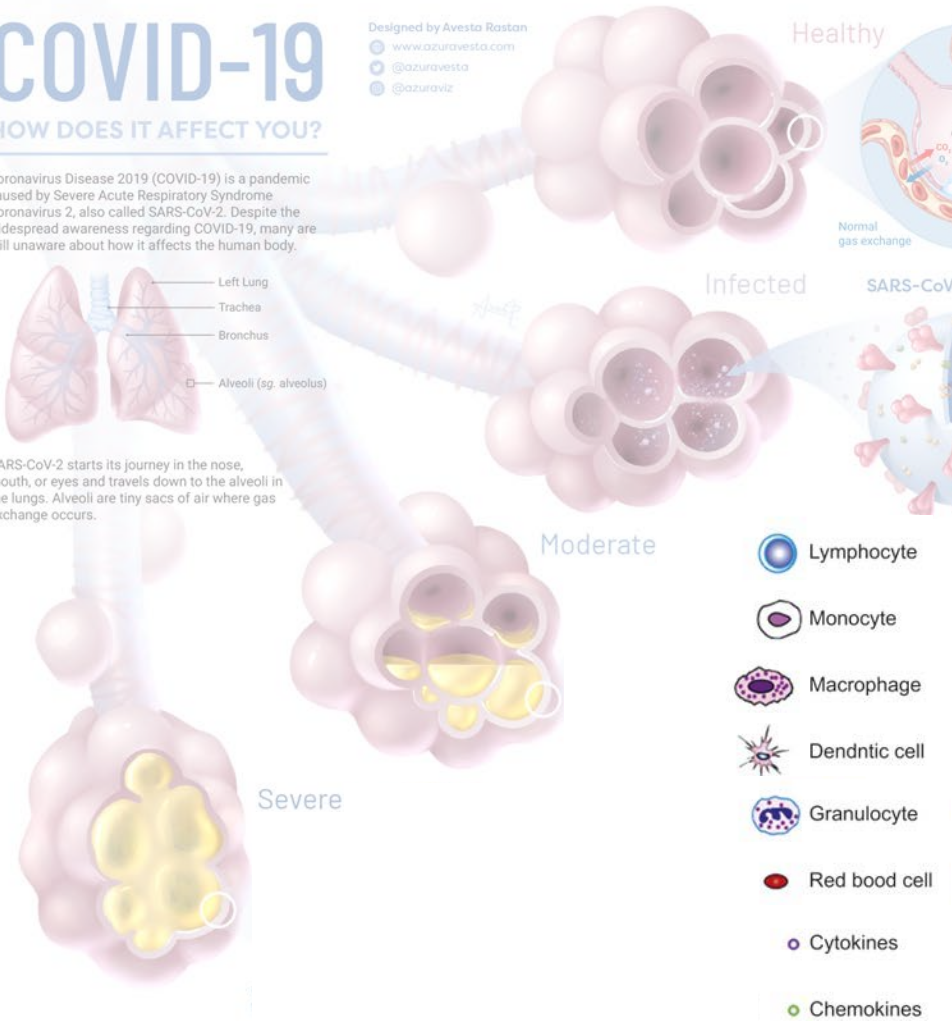
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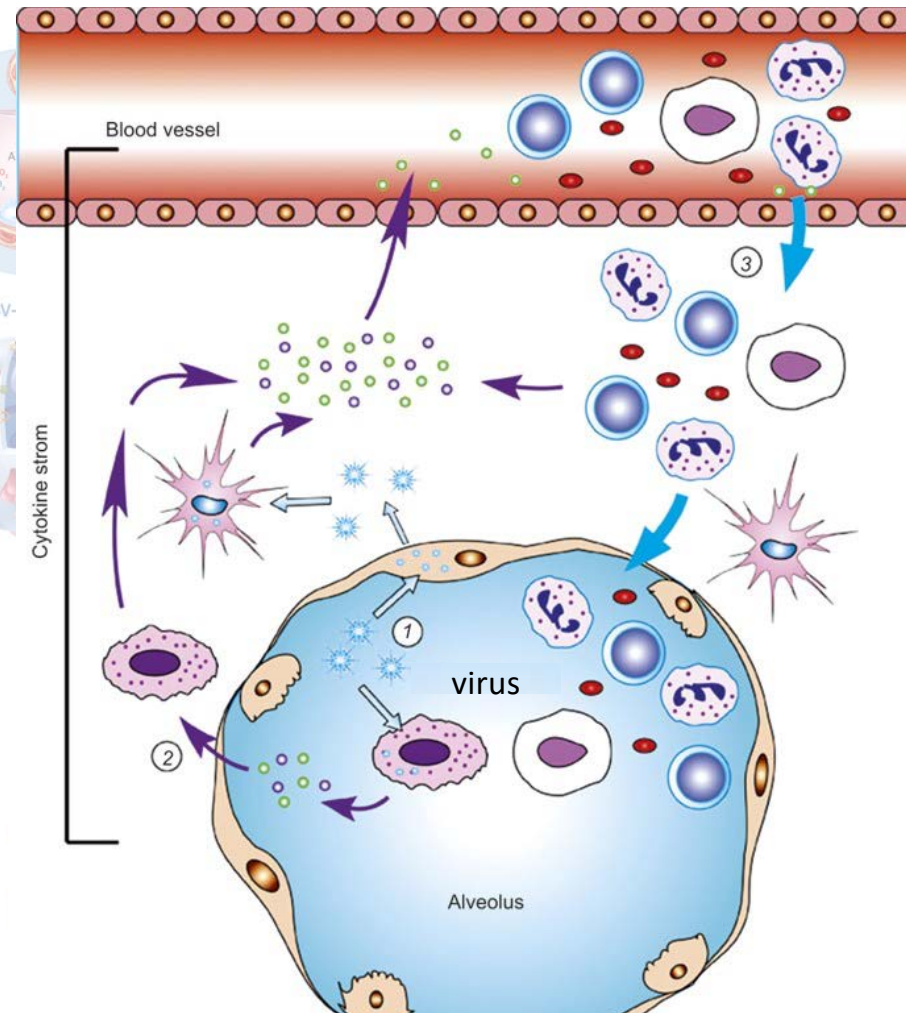


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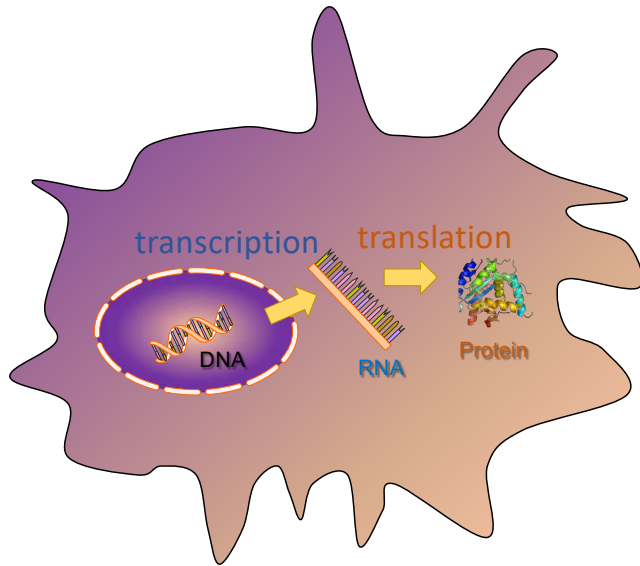


- Lymphocyte
- Monocyte
- Macrophage
- Dendritic cell
- Granulocyte
- Red blood cell
- Cytokines
- Chemokines

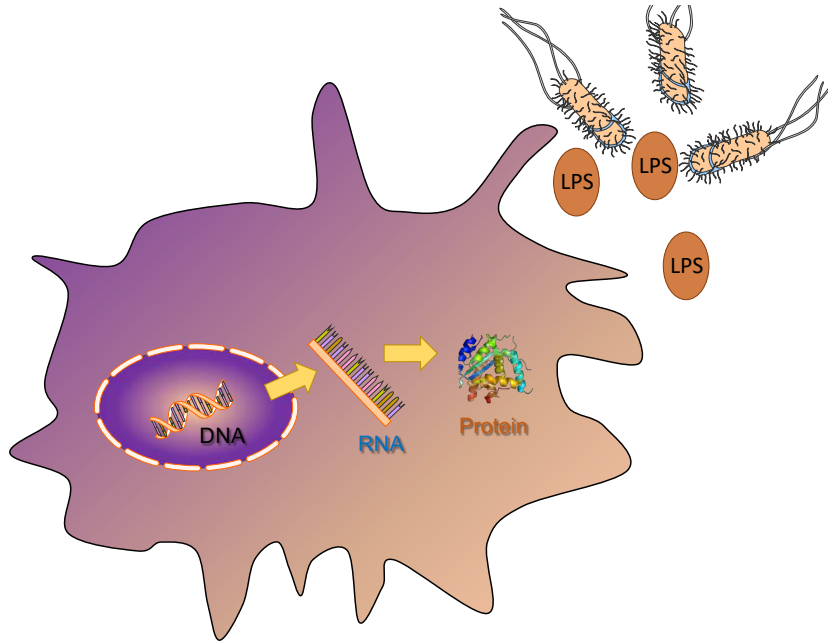


Liu, Q., Zhou, Y. & Yang, Z. The cytokine storm of severe influenza and development of immunomodulatory therapy. *Cell Mol Immunol* **13**, 3–10 (2016).

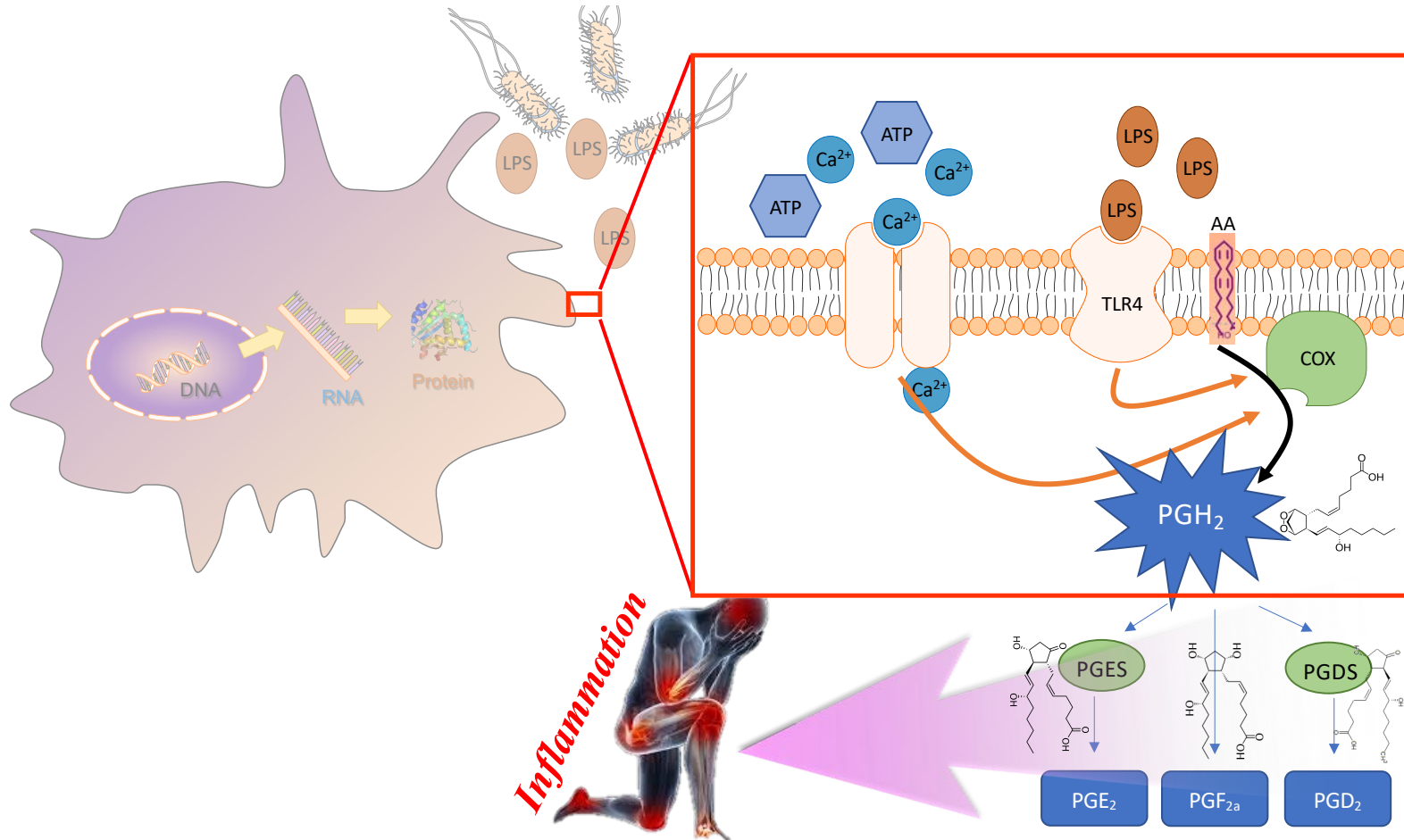
Mimicking the physiological response of Infection



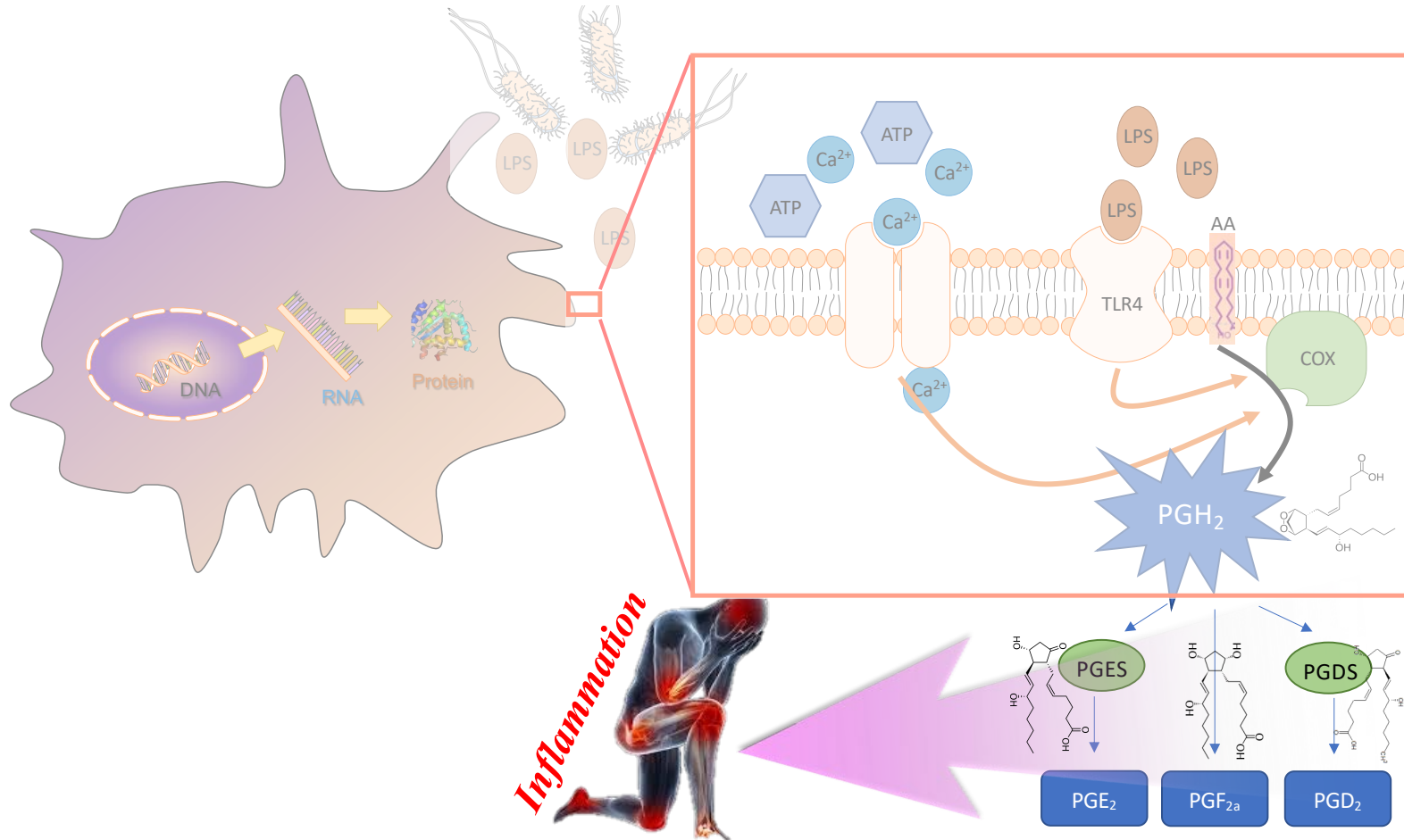
Mimicking the physiological response of Infection



Mimicking the physiological response of Infection



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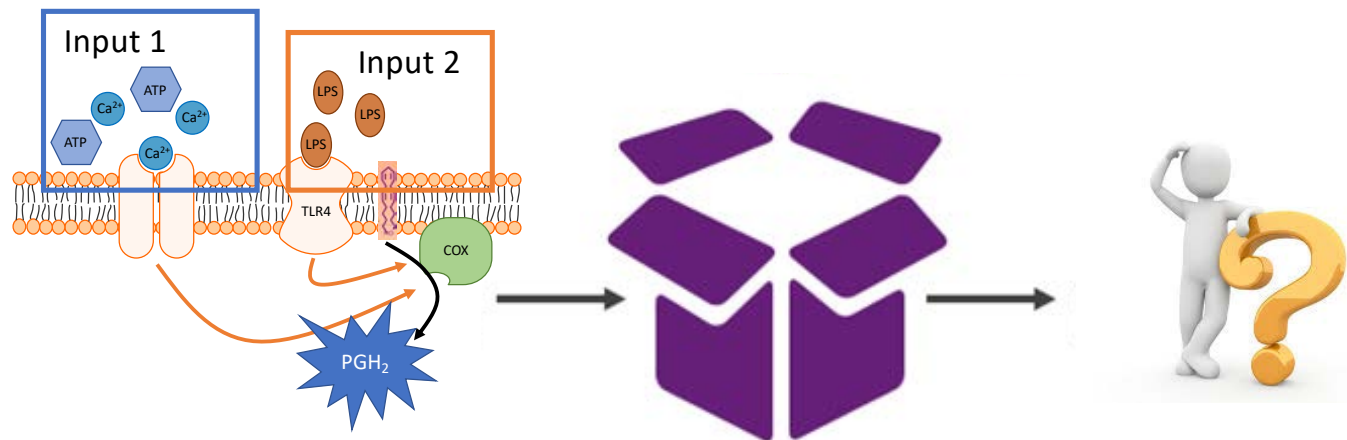
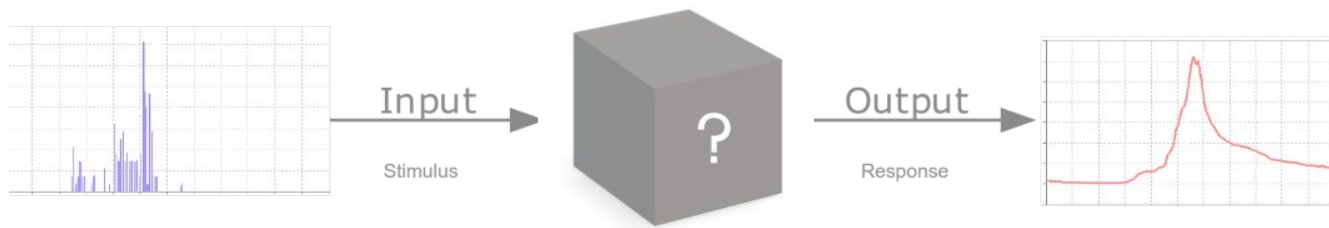


Standard Mathematical Modeling for Biological Networks

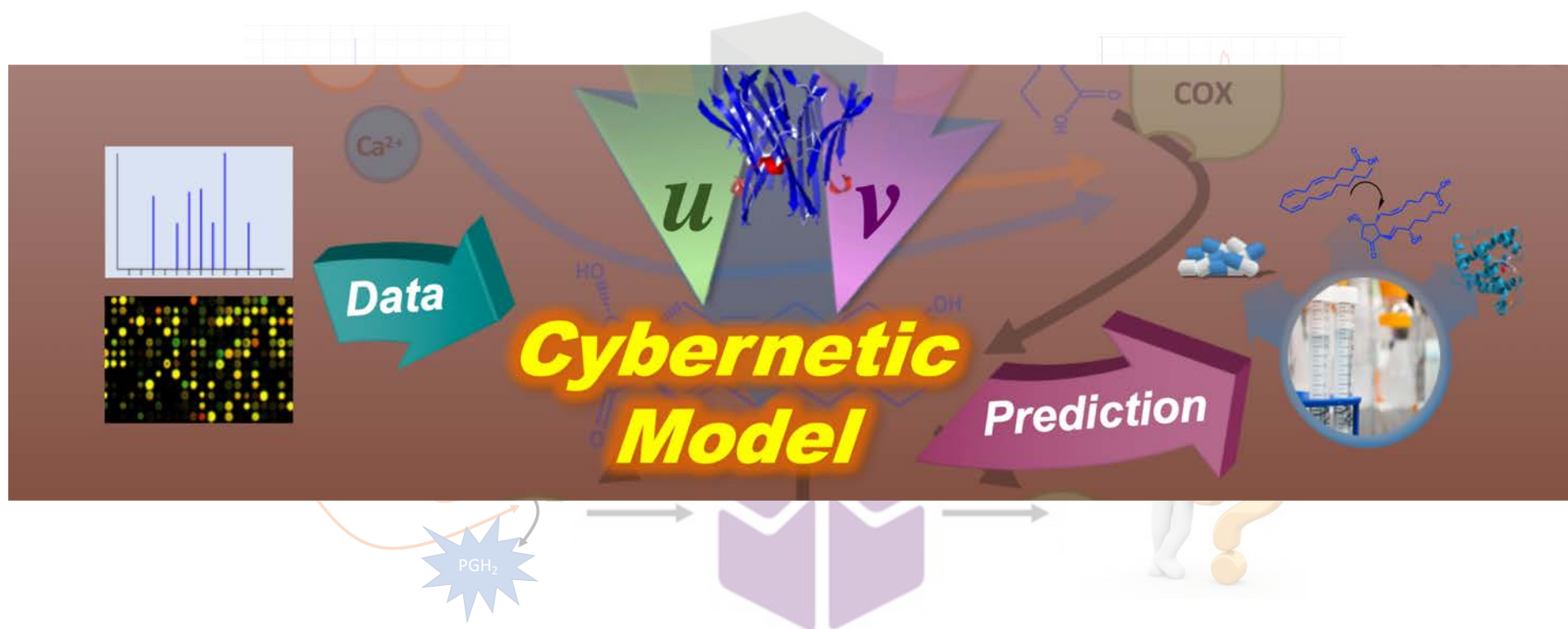
Standard Mathematical Modeling for Biological Networks



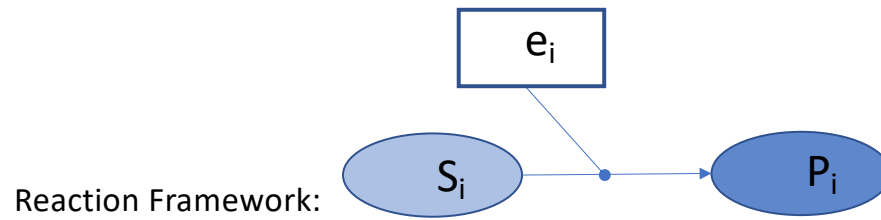
Standard Mathematical Modeling for Biological Networks



Alternate modeling framework: Cybernetic model



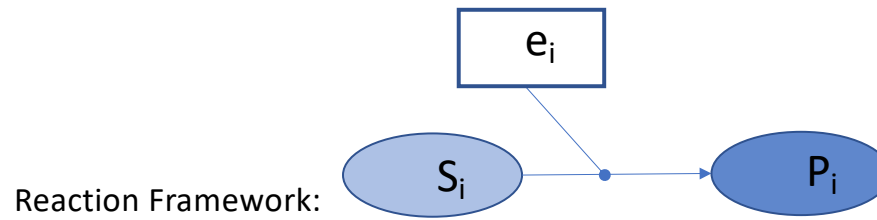
Reaction Kinetics



$$\frac{dP_i}{dt} = k_i e_i S_i - g_i P_i$$

$$\frac{de_i}{dt} = k_{e,i} S_i - \beta_{e,i} e_i$$

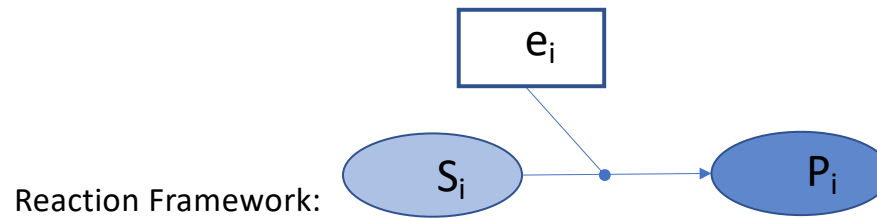
Introducing cybernetic control variables



$$\frac{dP_i}{dt} = v_i k_i e_i S_i - g_i P_i$$

$$\frac{de_i}{dt} = u_i k_{e,i} S_i - \beta_{e,i} e_i$$

Introducing cybernetic control variables

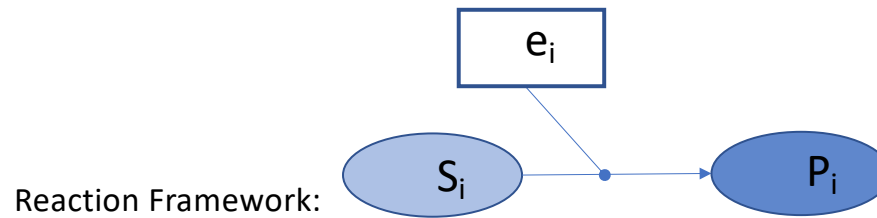


Activity Control

$$\frac{dP_i}{dt} = v_i k_i e_i S_i - g_i P_i$$

$$\frac{de_i}{dt} = u_i k_{e,i} S_i - \beta_{e,i} e_i$$

Introducing cybernetic control variables



$$\frac{dP_i}{dt} = v_i k_i e_i S_i - g_i P_i$$

$$\frac{de_i}{dt} = u_i k_{e,i} S_i - \beta_{e,i} e_i$$

Synthesis Control

Defining cybernetic control variables

Goal: Survival

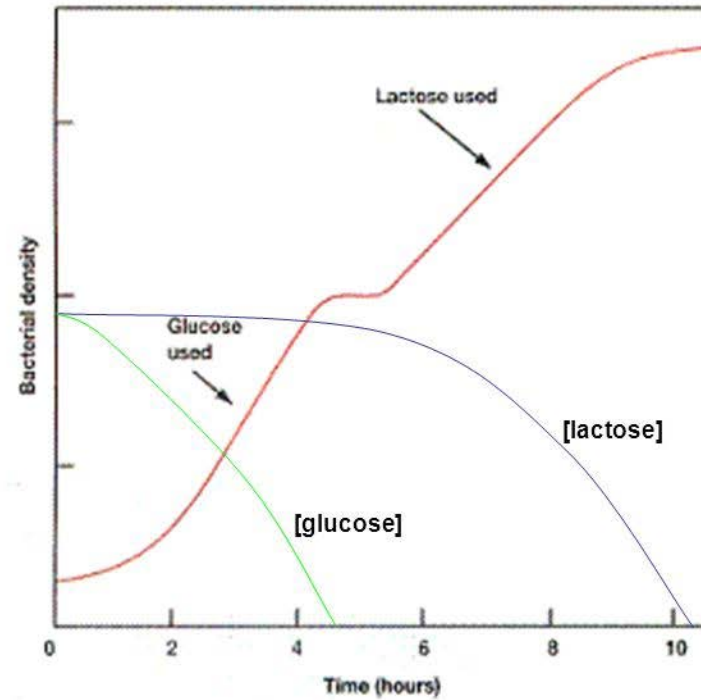
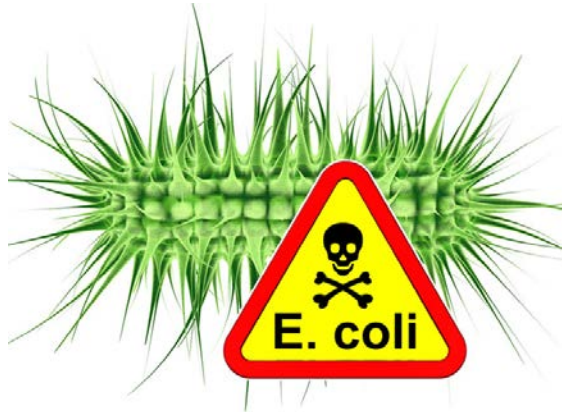
Specific goal: Maximize biomass production rate within available resources

Return on investment: $\rho_i = r_{S_i \rightarrow P_i}^{unregulated} = k_i e_i S_i$

$$v_i = \frac{\rho_i}{\max_j \rho_j}$$

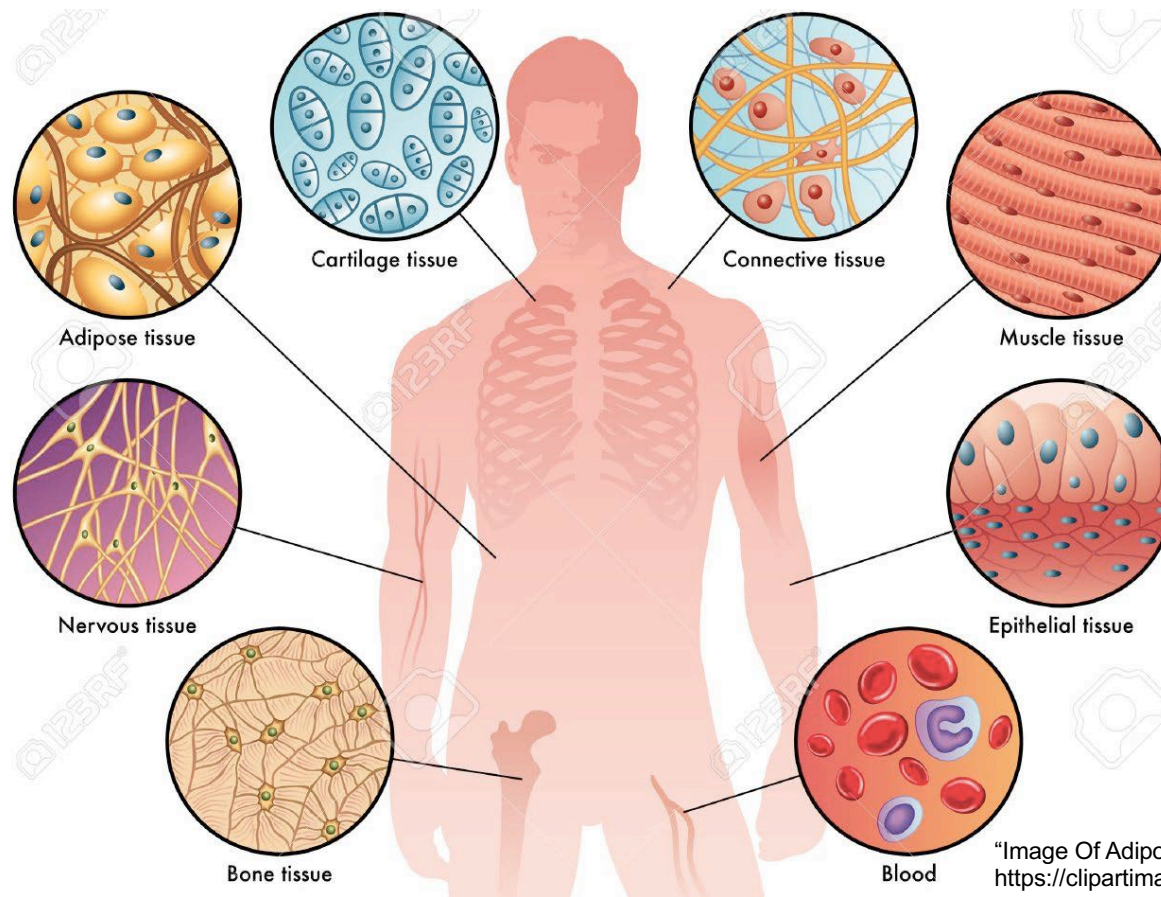
$$u_i = \frac{\rho_i}{\sum_j \rho_j}$$

Diauxic growth of E. coli



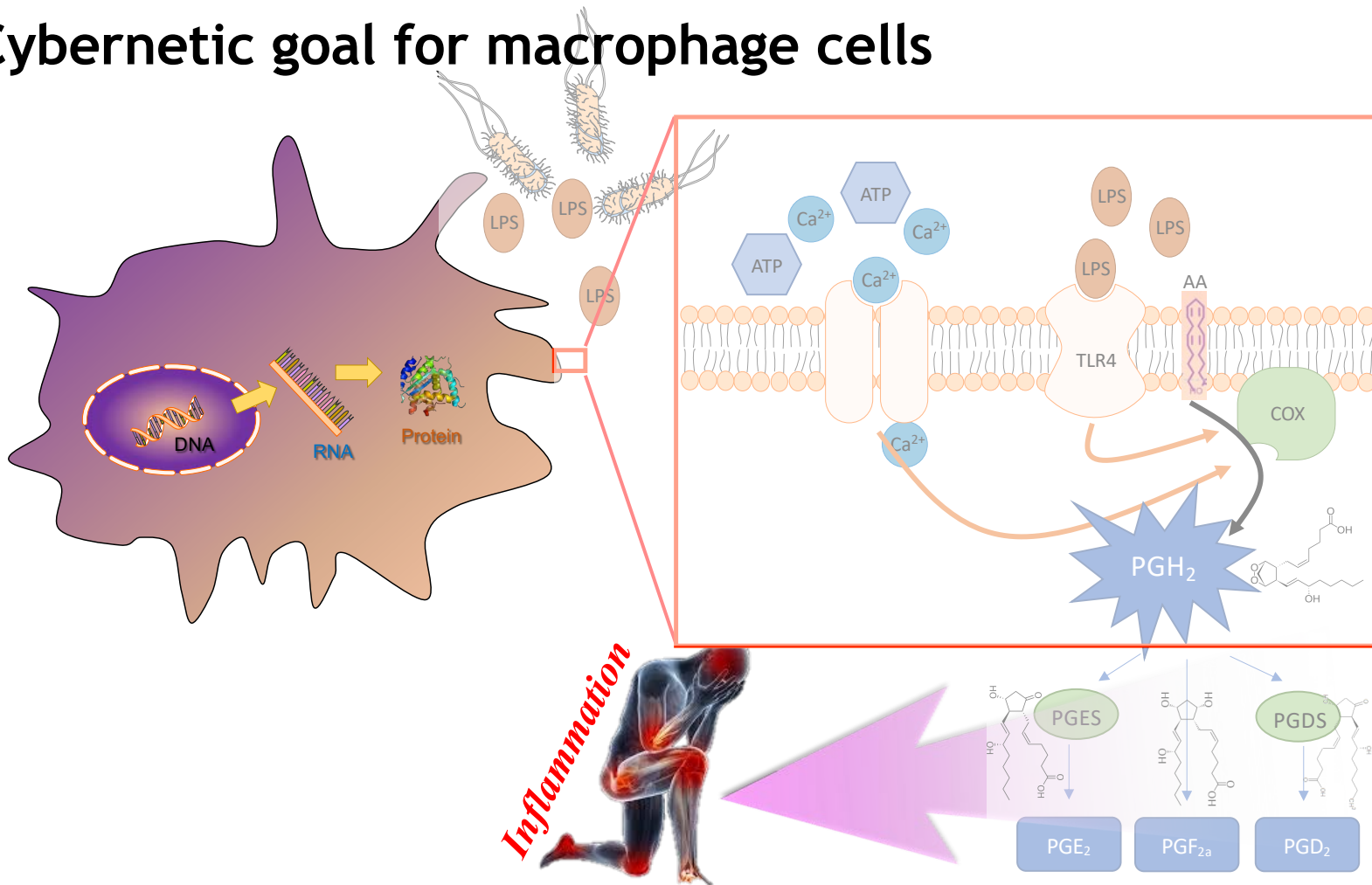
Kompala, D.S., et al., *Investigation of bacterial growth on mixed substrates: experimental evaluation of cybernetic models*. Biotechnol Bioeng, 1986. 28(7): p. 1044-55.

Multicellular Systems

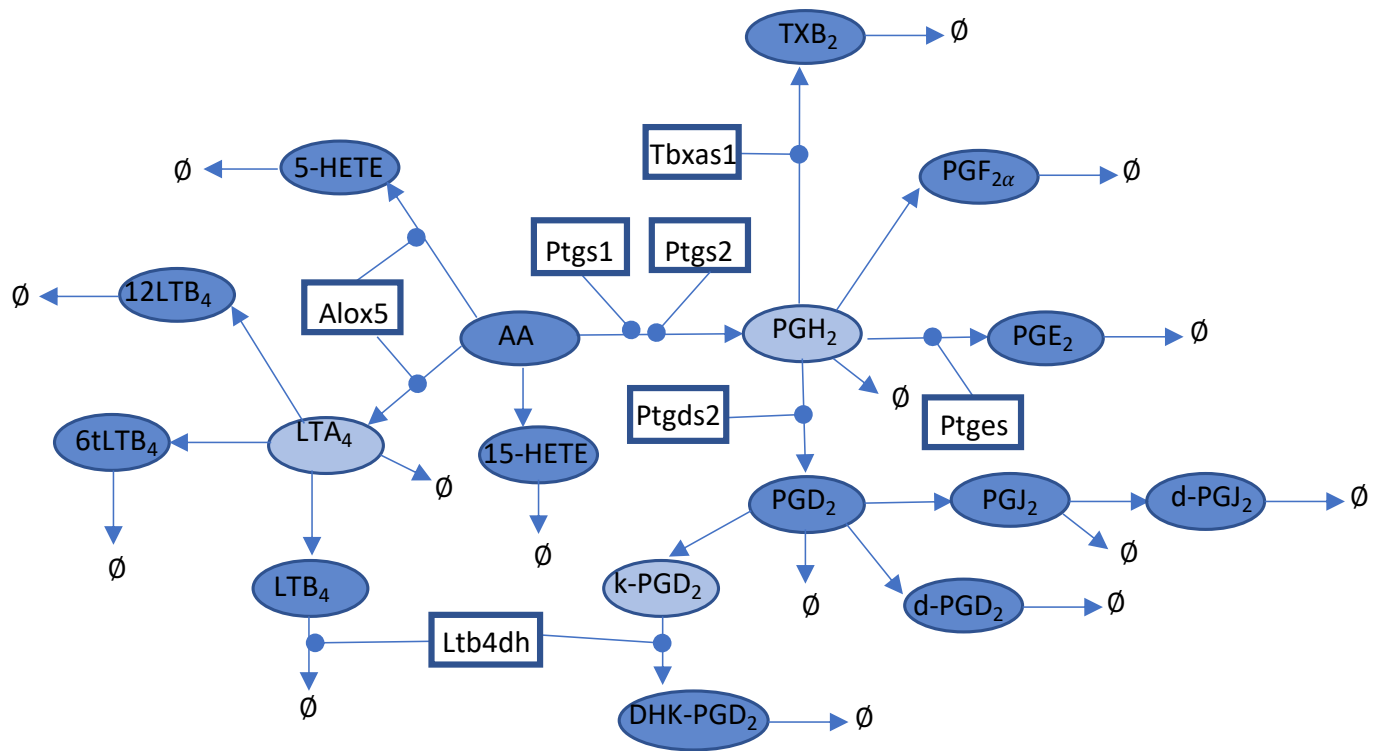


"Image Of Adipose Tissue In A Human Body Clipart"
<https://clipartimage.com/images/clipart-367516.html>

Cybernetic goal for macrophage cells

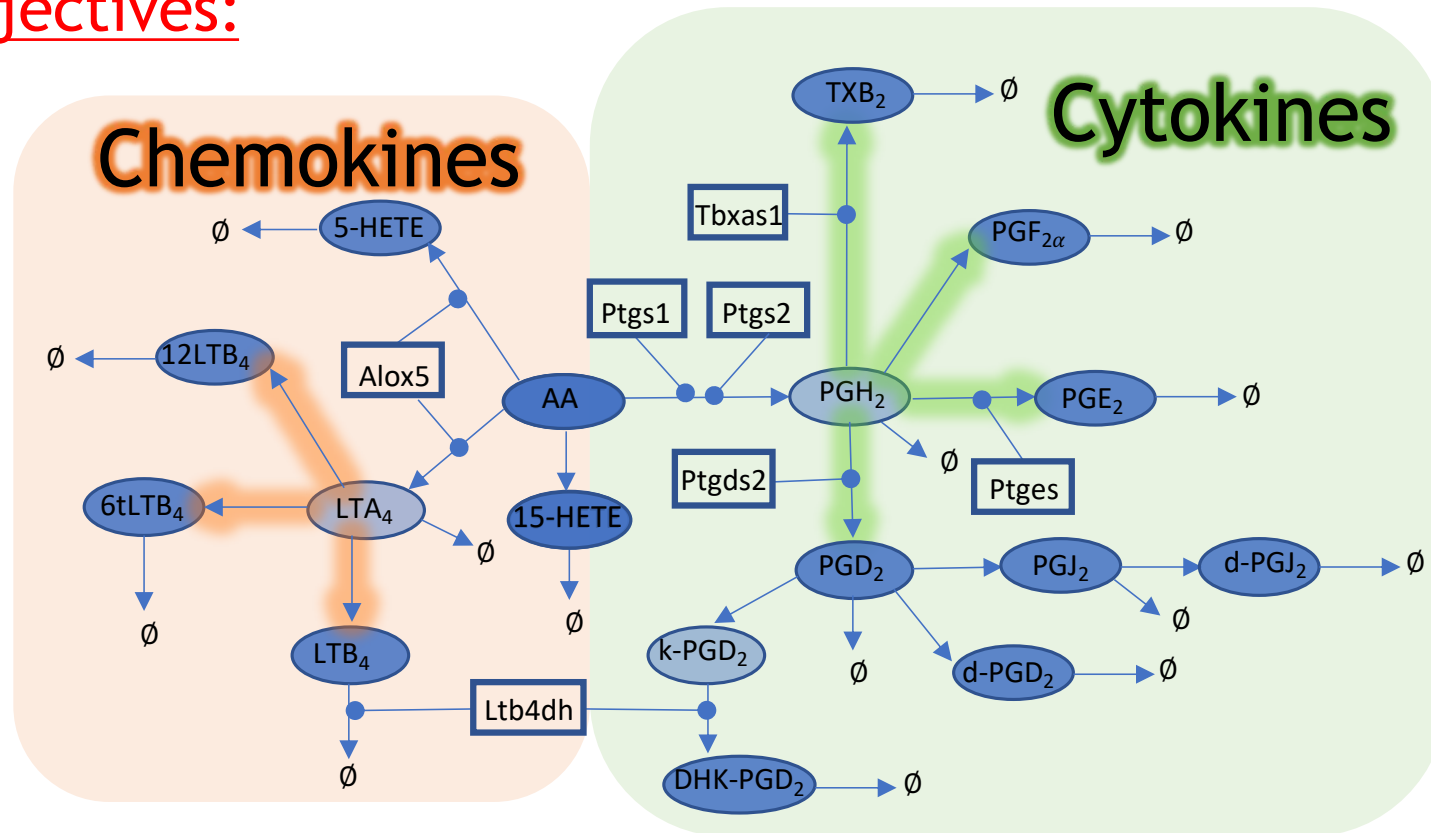


Eicosanoid Metabolism

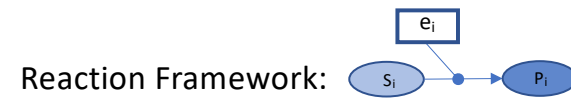
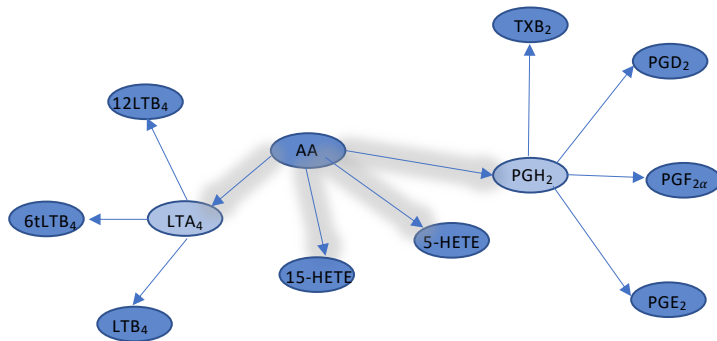


Cybernetic Model of Eicosanoid Metabolism

2 objectives:



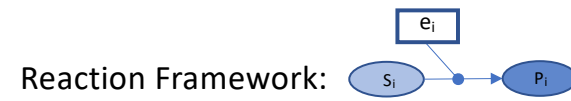
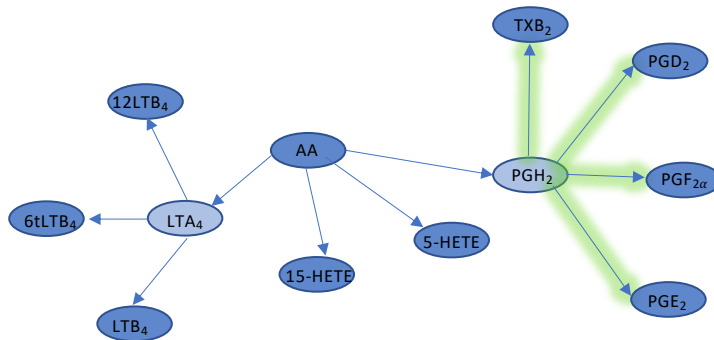
Part1: Kinetic model



$$\frac{dP_i}{dt} = k_i e_i S_i - g_i P_i - (\text{downstream fluxes})$$

$$\frac{de_i}{dt} = k_{e,i} S_i - \beta e_i$$

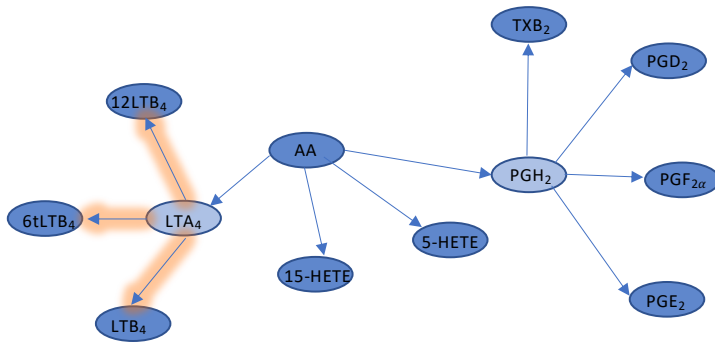
Part2: Cybernetic Regulation with **Cytokines**



$$\frac{dP_i}{dt} = v_i k_i e_i S_i - g_i P_i - (\text{downstream fluxes})$$

$$\frac{de_i}{dt} = u_i k_{e,i} S_i - \beta e_i$$

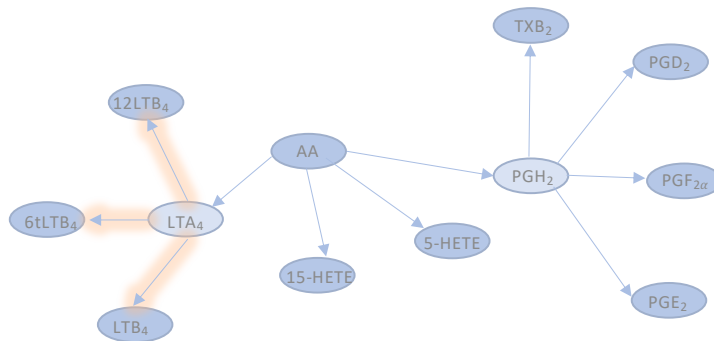
Part3: Cybernetic Regulation with Chemokines



$$\frac{dP_i}{dt} = v_i k_i e_i S_i - g_i P_i - (\text{downstream fluxes})$$

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Enzyme Synthesis Control

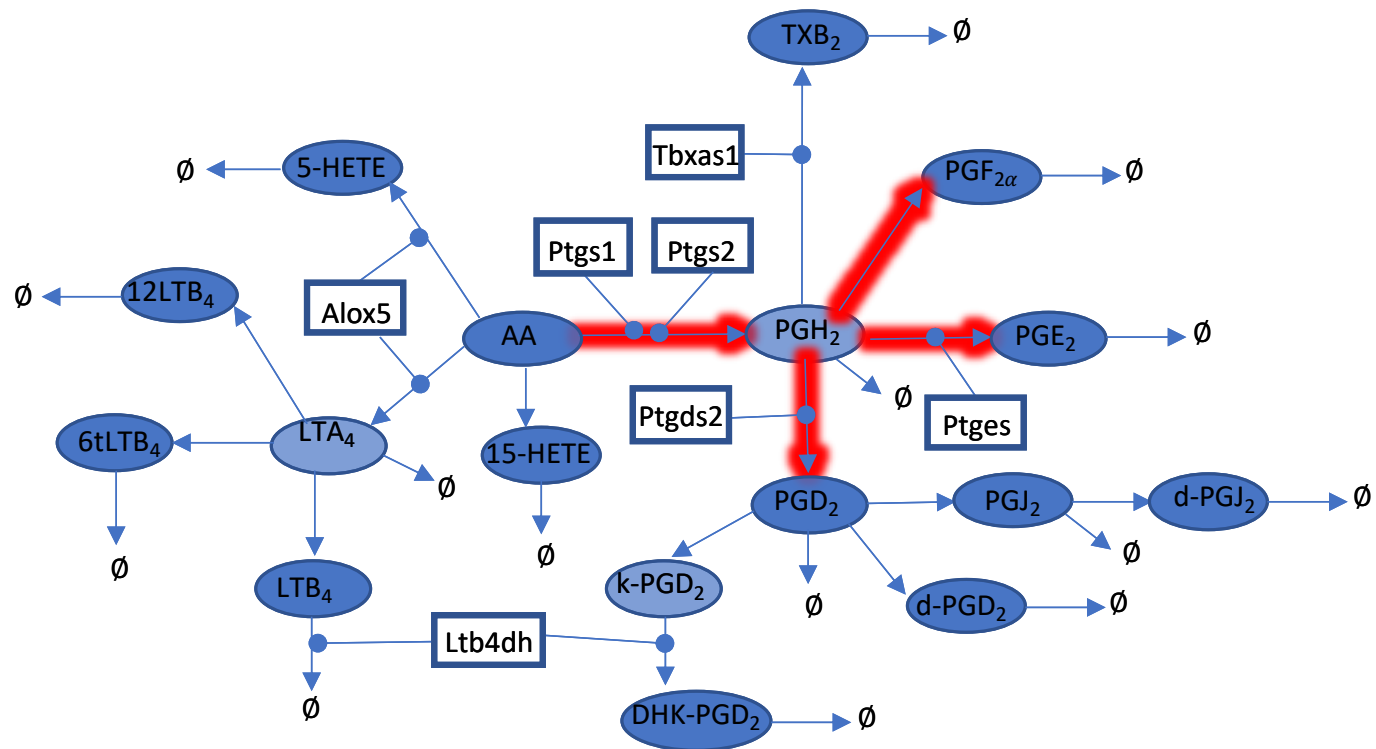
$$u_i = \frac{\rho_i}{\sum_j \rho_j}$$

Enzyme Activity Control

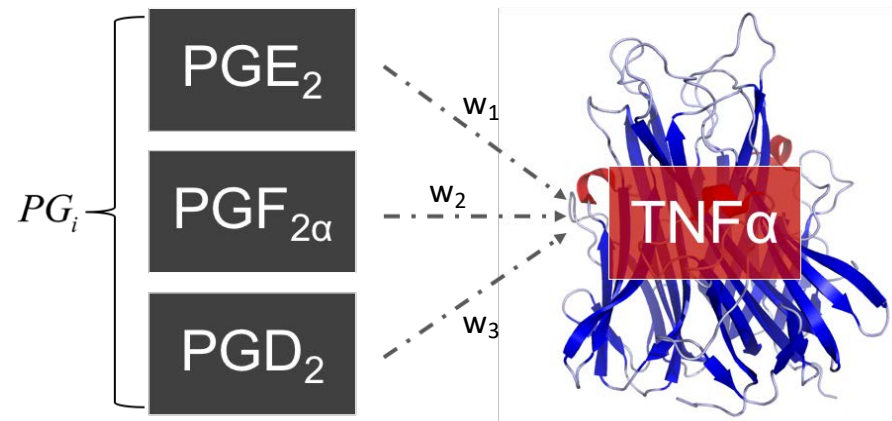
$$v_i = \frac{\rho_i}{\max_j(\rho_j)}$$

*What about the Cybernetic Goal
& How do we calculate $\rho_i = ?$*

A closer look at Part 2



Defining the Cybernetic Goal



$$TNF\alpha = \sum_i w_i PG_i$$

The Cybernetic Variables

GOAL: “dynamically maximize $TNF\alpha$ ”

$$TNF\alpha = \sum_i w_i P G_i$$

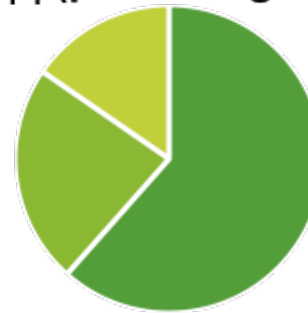
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$$\rho_i = w_i r_{PGH_2 \rightarrow PG_i}^{unregulated}$$

Relative Contribution to Product
 $w_i r_i$ (pmol/s/ugDNA)



Pathway

● PGE₂ ● PGF_{2α} ● PGD₂

The Cybernetic Variables

GOAL: “dynamically maximize $TNF\alpha$ ”

$$TNF\alpha = \sum_i w_i PG_i$$

$$\rho_i = w_i r_{PGH_2 \rightarrow PG_i}^{unregulated}$$

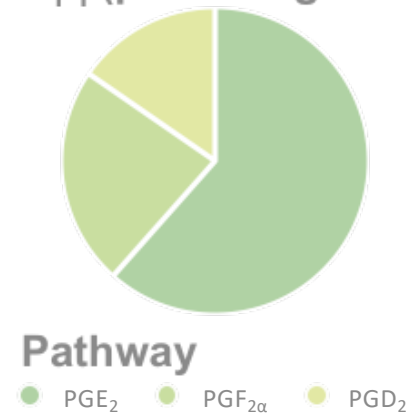
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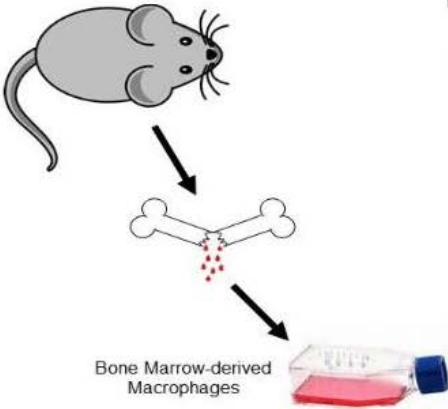
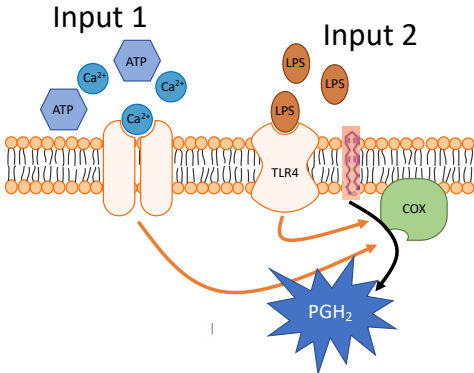
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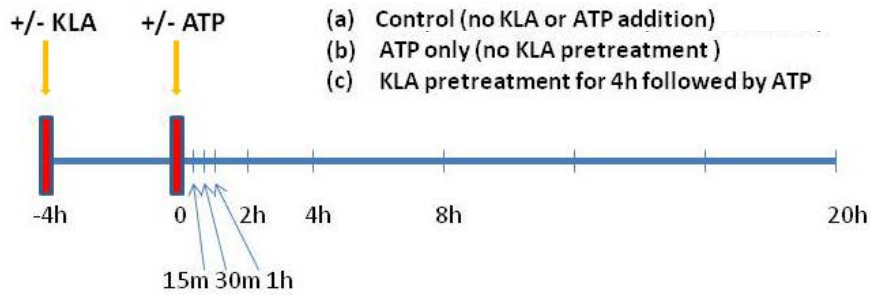


System Properties

Cell type:
Bone Marrow-Derived Macrophages



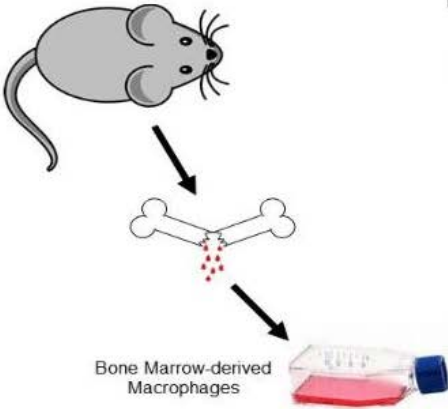
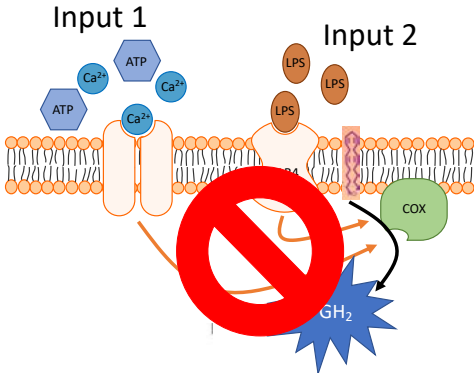
KLA/ATP timecourse on BMDM's: Experimental design



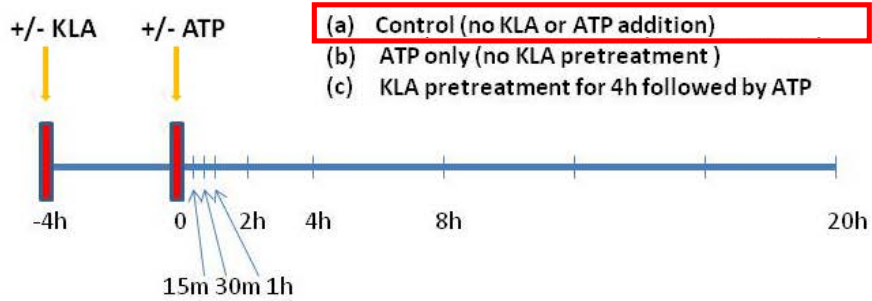
Lipid/mRNA measurements taken at 0 (ctrl only), 15m, 30m, 1h, 2h, 4h, 8h, 20h (relative to ATP addition)

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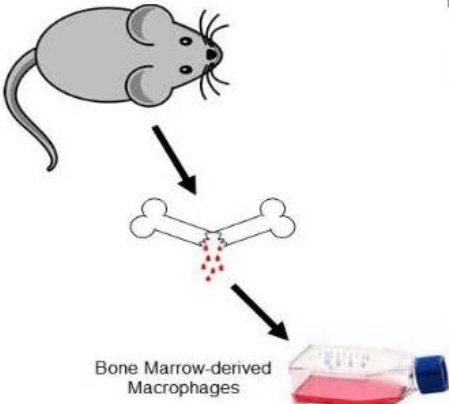
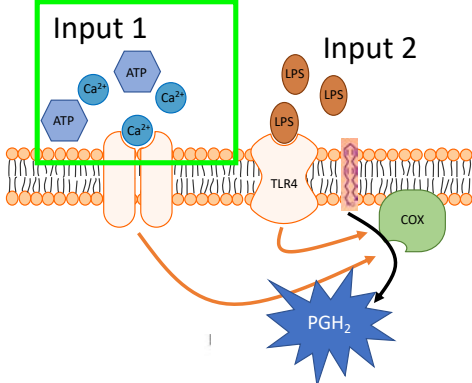
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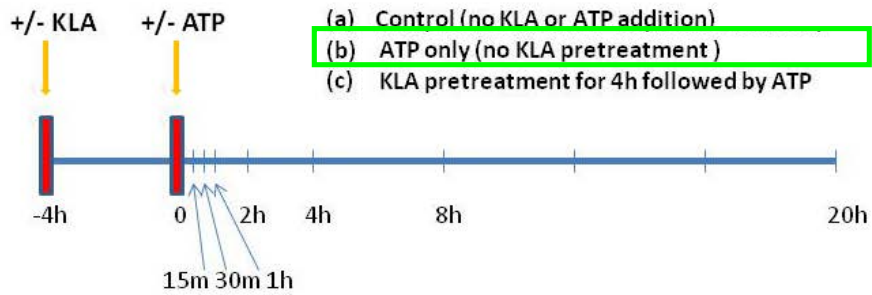
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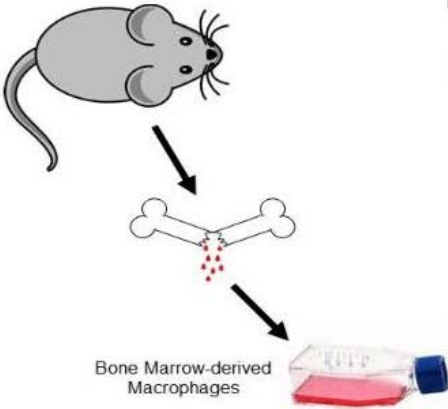
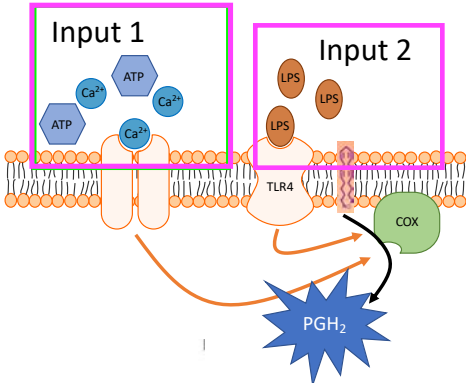
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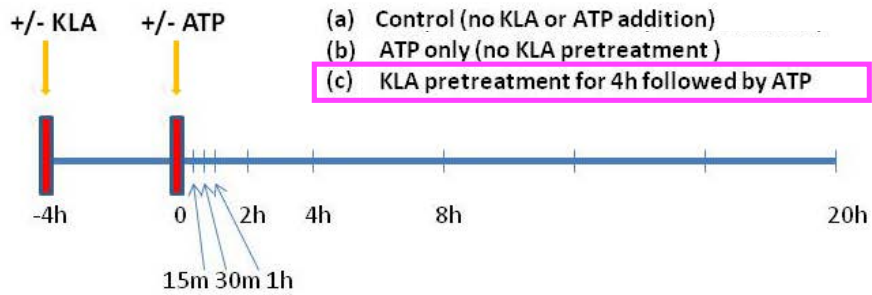
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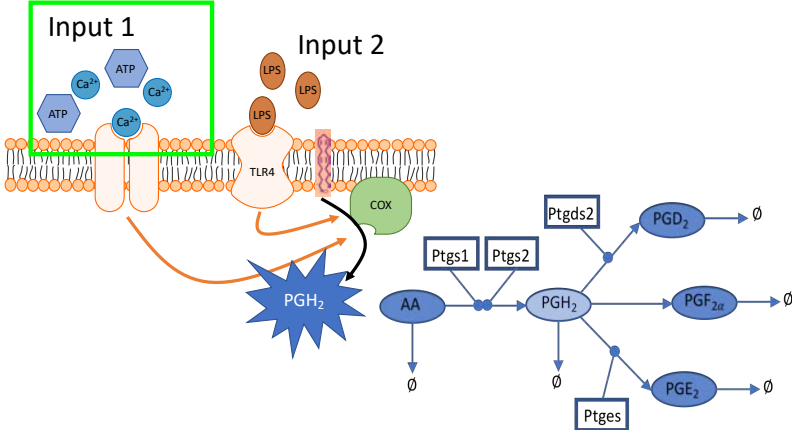


KLA/ATP timecourse on BMDM's: Experimental design

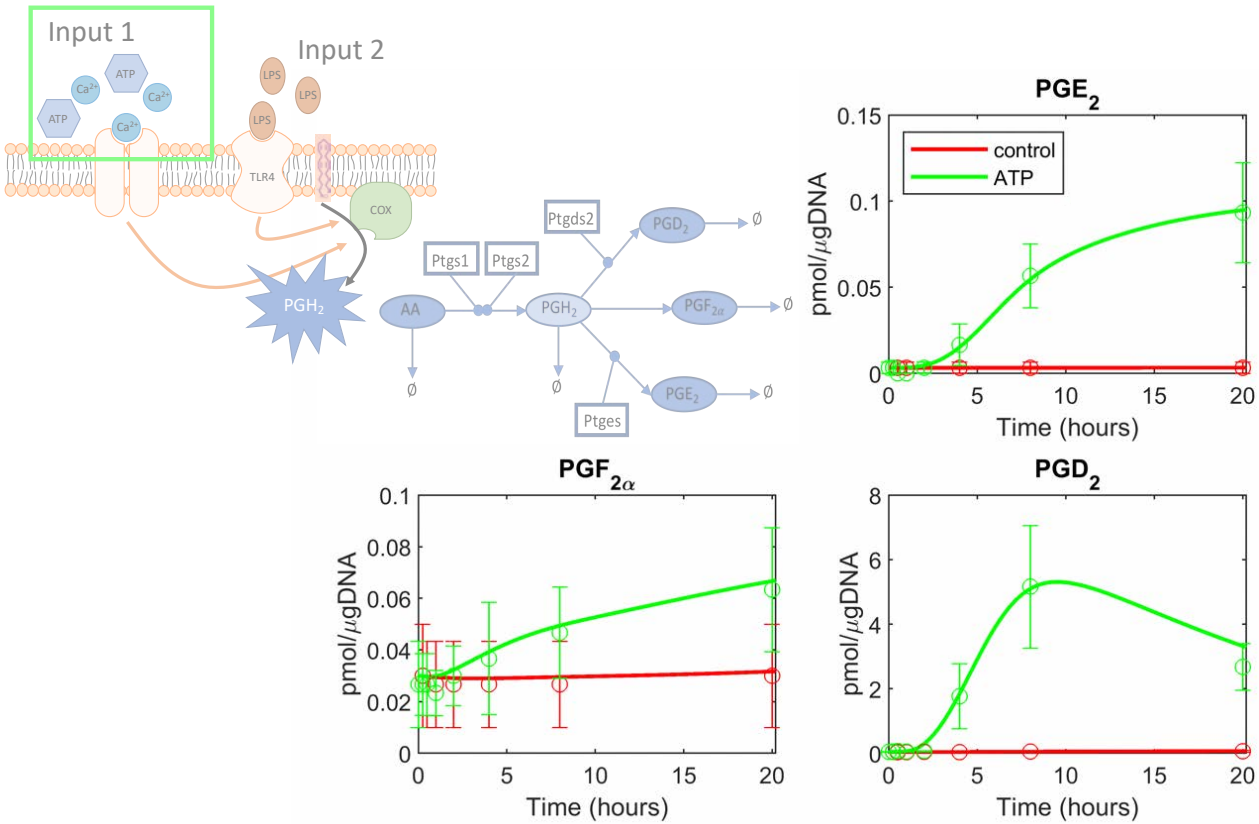


Lipid/mRNA measurements taken at 0 (ctrl only), 15m, 30m, 1h, 2h, 4h, 8h, 20h (relative to ATP addition)

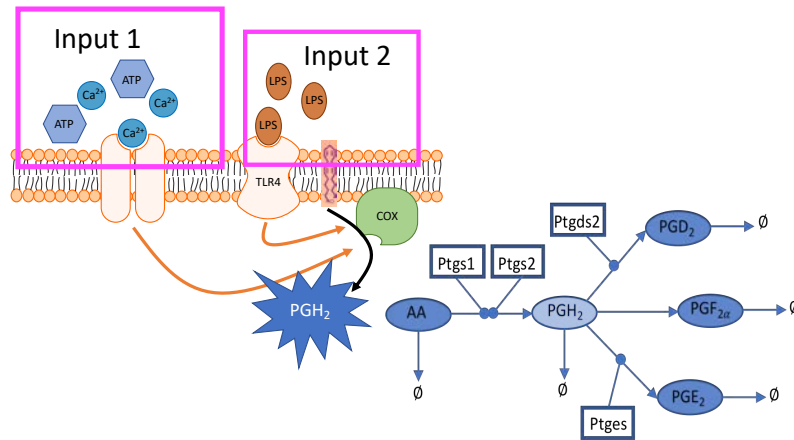
Parameter Estimation: Simulating ATP Stimulated BMDM Cells



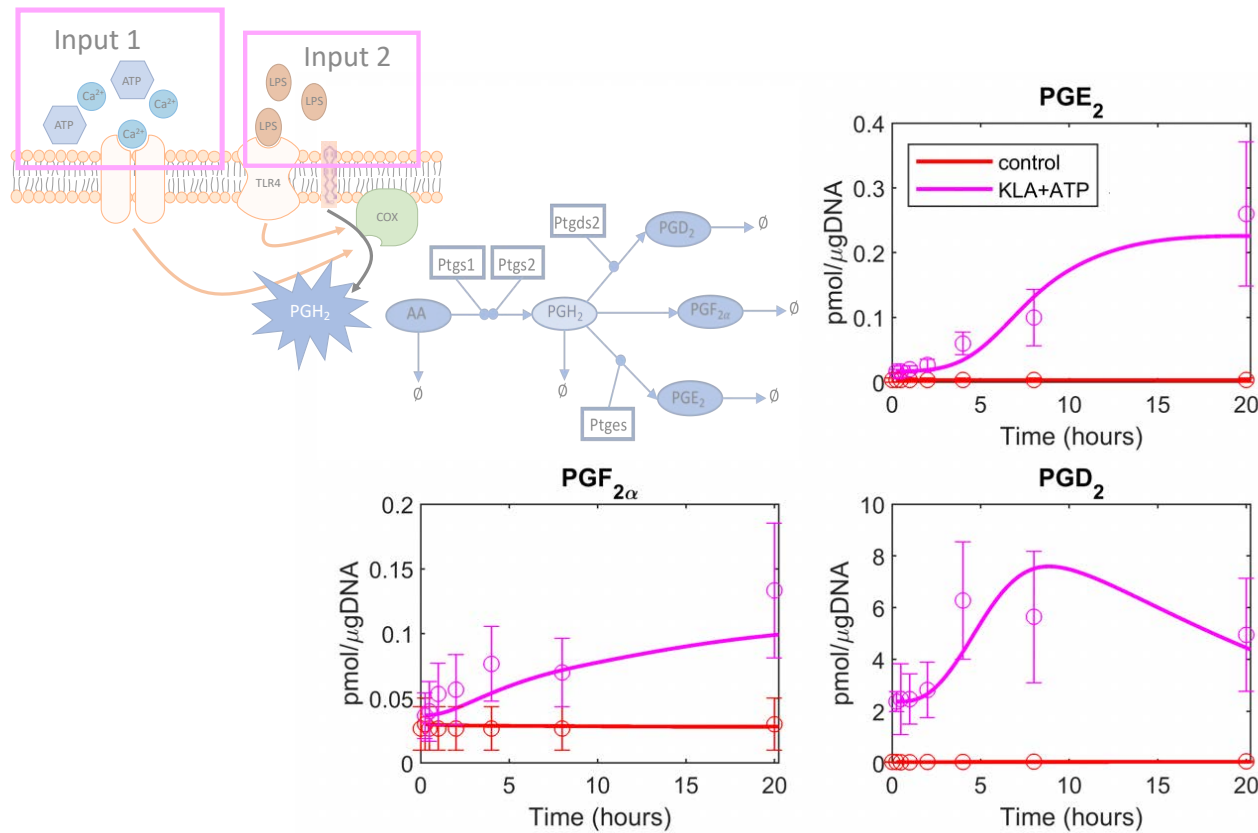
Parameter Estimation: Simulating ATP Stimulated BMDM Cells



Model Validation: Predicting KLA Primed & ATP Stimulated BMDM Cells

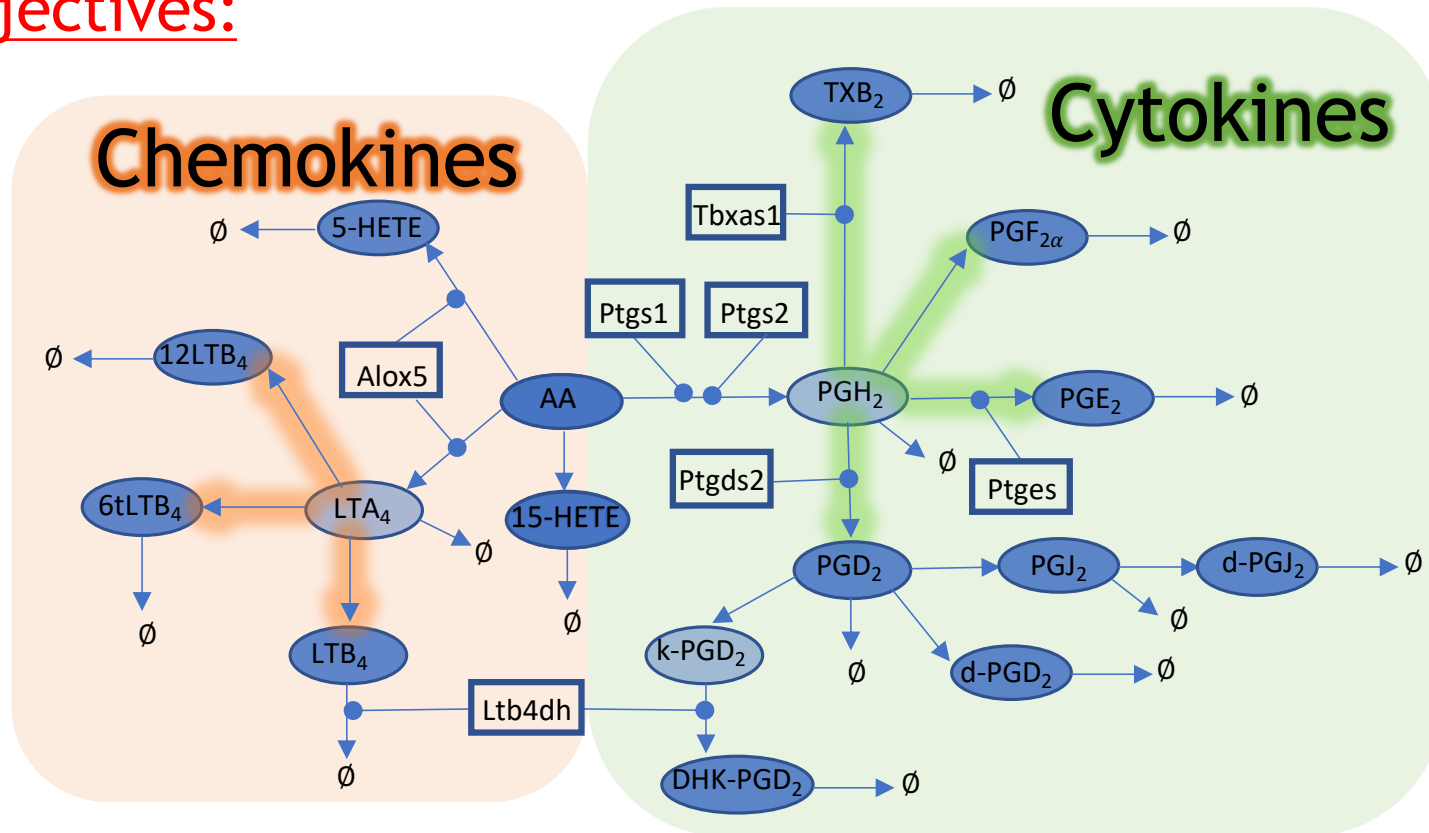


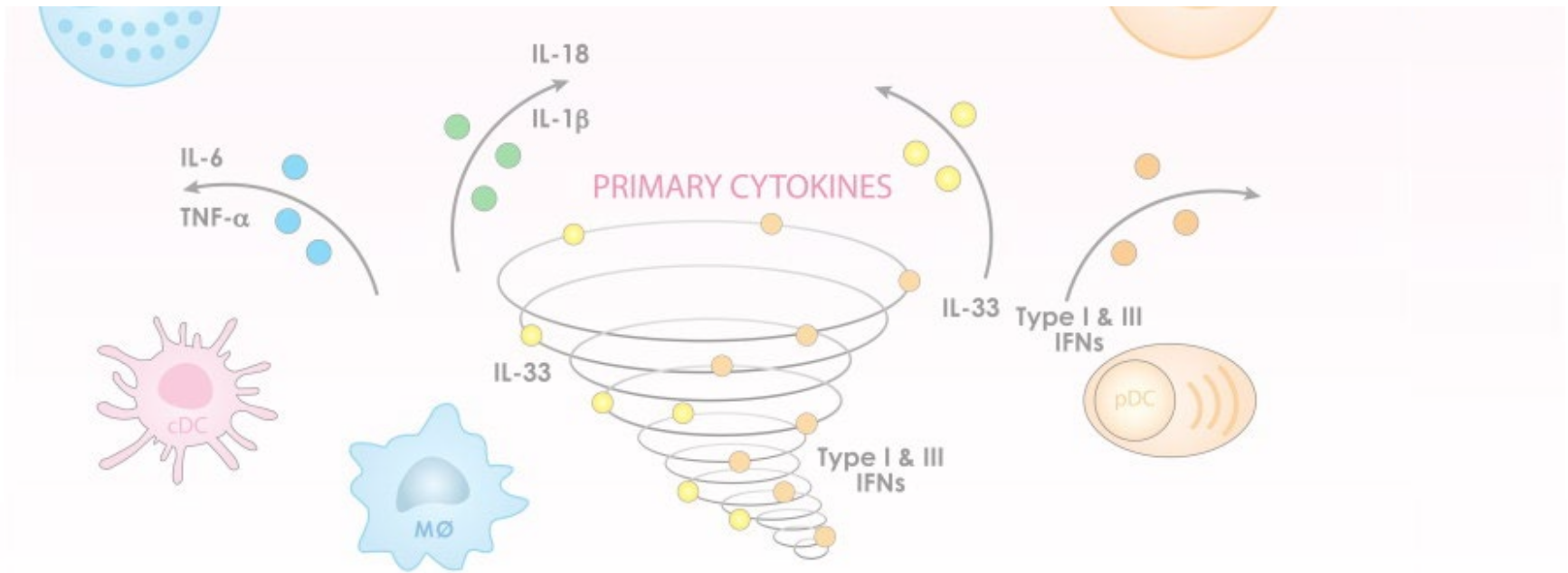
Model Validation: Predicting KLA Primed ATP Stimulated BMDM Cells



Cybernetic Model of Eicosanoid Metabolism

2 objectives:

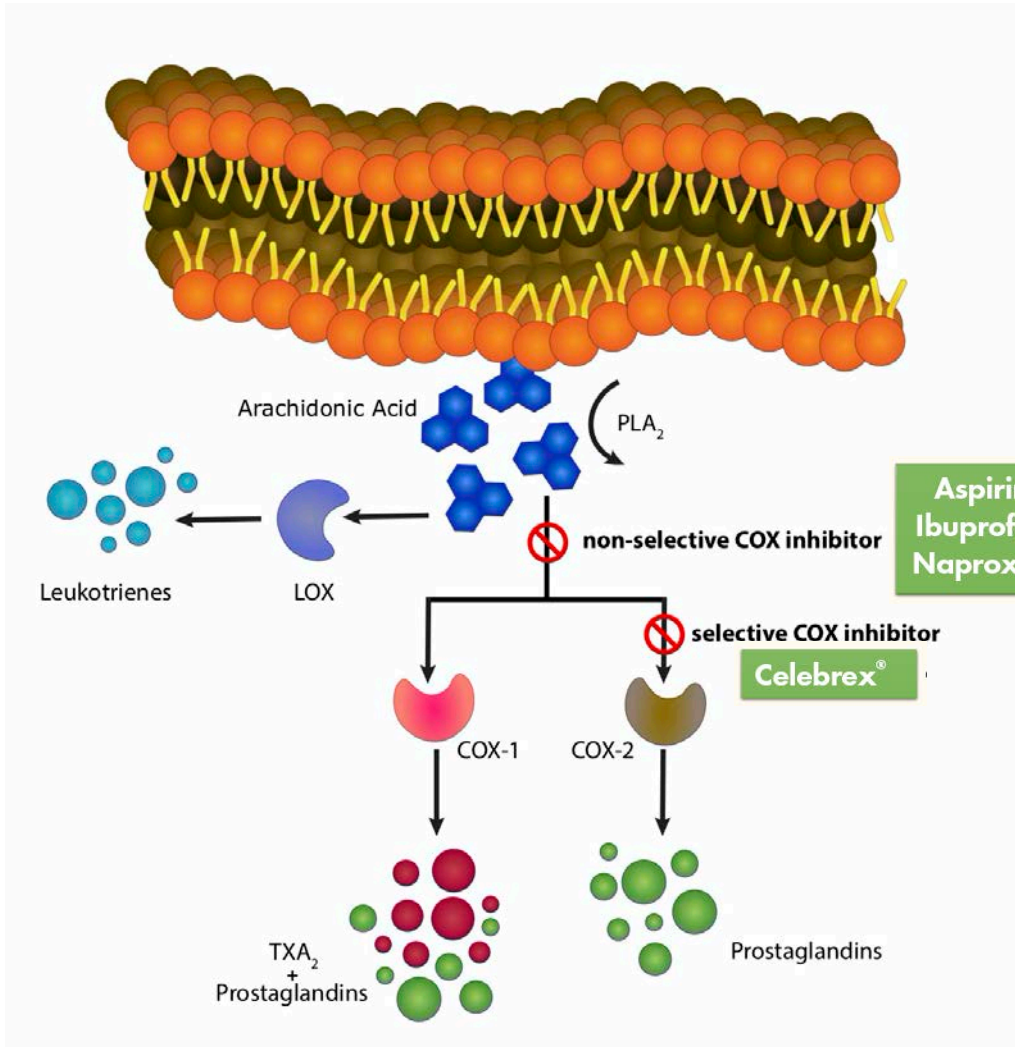




Cytokine storm and NSAIDS?
 How can modeling help?



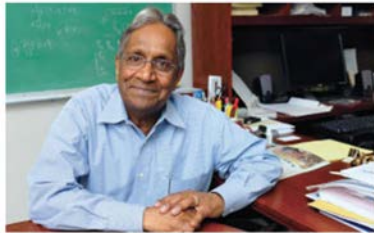
NSAIDs and COX



Special thanks to...



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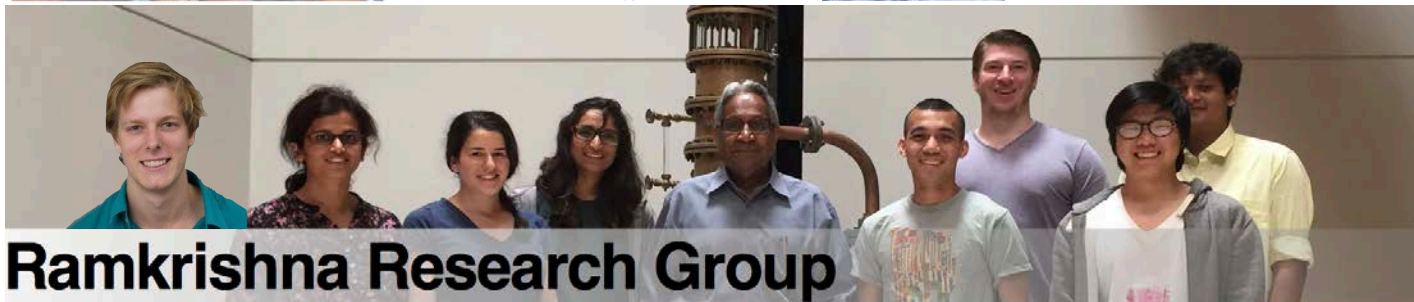


Dr. Doraiswami Ramkrishna
Harry Creighton Peffer
Distinguished Professor



Dr. Shankar Subramaniam
Distinguished Professor of
Bioengineering, Bioinformatics
and Systems Biology

UC San Diego
JACOBS SCHOOL OF ENGINEERING



Ramkrishna Research Group



Subramaniam Lab Research Group

Questions?

A Cybernetic Approach to Modeling Lipid Metabolism in Mammalian Cells.
Processes 2018, 6(8),126; <https://doi.org/10.3390/pr6080126>



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